



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/660,499
Source: 1/FWJ0
Date Processed by STIC: 2/24/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS..

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004
TIME: 09:43:29

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

3 <110> APPLICANT: Seoul National University Industry Foundation
5 <120> TITLE OF INVENTION: ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
6 AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
8 <130> FILE REFERENCE: 20020-02USA
10 <140> CURRENT APPLICATION NUMBER: US 10/660,499
11 <141> CURRENT FILING DATE: 2003-09-12
13 <150> PRIOR APPLICATION NUMBER: KR 2003-19069
14 <151> PRIOR FILING DATE: 2003-03-27
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: KopatentIn 1.71

ERRORED SEQUENCES

225 <210> SEQ ID NO: 9
226 <211> LENGTH: 29
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Primer
234 <400> SEQUENCE: 9
235 accaagcttg gagttgtatgg gaataatca
E--> 239 ① delete

29

pp 1-4
Does Not Comply
Corrected Diskette Needed

see pp 2-3 for more errors

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<400> 1
gcacgagctt caaccctctca tcattaggca ttcagcaagc aaaaaaaaaa a 51
atg ✓ ggc✓aaa✓atc✓atg ✓ ctt ✓ gtt ✓ ttg✓ggt✓ agc✓ctc att ✓ gga tta ✓ tgt 99
Met Gly → Lys → Ile → Met → Leu → Val → Leu → Gly → Ser → Leu → Ile → Gly → Leu → Cys → Cys
1 One Space 5 10 One Space 15
ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc 147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
20 25 30

sample of invalid amino acid placement
in sequence 1.

Per 1.822 of Sequence Rules, insert only one space
between codons and amino acids; also, place amino acid
directly under its codon

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<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 3 see p. 4 for error explanation
n(gggatccga ygc(t)ggm a(cha)tgggyg g(y)gctg(y)gt a(ngg)

44

<210> 4
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4 see p. 4
n(y)gatcctt kswytgccar ttnnshcccc artthnck 37

<210> 5
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 5 see p. 4
gaygcwswng gnachatggg n(ggg)ntgy ggntayggm ayytntaygc ha(ngg)ntay 60
ggachmoga cngc(g)cyt t(w)achngd ytttyaayg ayggggcws t(g)ggncar 120
tgytayaara thathtgya ytayaarwsn gayws(m)nt ggtgyathaa rgqnmgnwsn 180
gtmacngtha cngcmacnaa yttytgycn(c) cn(a)ayttg cm(y)ncnaa yaayaaygn 240
ggnctggtya ayconcnnyt haarcaytty gayatggcnc arccongntg ggaraarath 300
gg(n)athtaym qngonggnat hgtncngtn ytnntycarm qngtncntg yaaraarcay 360
ggngngn(t)n qnntywsgt haayggmogn gaytayttyg arytnqtnyt mathwsnhaay 420
gtngngngng dnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac (ngg)ntggatg 480
gnatgwsm gnaytggg mwsnaaytgg carwsnay 519

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004
TIME: 09:43:30

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

Err explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 1,2,14,17,20,23,42

Seq#:4; N Pos. 1,2,23,24,26,35

Seq#:5; N Pos. 6,9,12,15,21,24,27,33,39,45,51,54,57,63,66,69,72,75,78,81,84

Seq#:5; N Pos. 87,90,93,105,108,111,117,150,156,159,174,177,180,183,186,189

Seq#:5; N Pos. 192,195,198,210,213,222,225,228,240,243,255,258,261,279,285

Seq#:5; N Pos. 288,303,312,315,318,324,327,330,333,342,345,348,363,366,369

Seq#:5; N Pos. 372,378,381,387,390,405,408,411,417,423,426,429,432,435,438

Seq#:5; N Pos. 447,450,462,465,471,474,483,489,492,501,504,516

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004
TIME: 09:43:30

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
L:139 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:152 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
L:152 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:165 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:165 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:239 M:254 E: No. of Bases conflict, this line has no nucleotides.